



1/ 20

1 60
GTCCCTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTTCTCTGTCTGCGCGCTG
-----+-----+-----+-----+-----+-----+-----+-----+
CAGGAAGGTGCTACGTGAGCGACCCGAAGAAGAGACACCGCACAAAGAGACGAGCGGCGAC
M H S L G F F S V A C S L L A A A
120
CGCTGCTCCCGGGTCTCGCGAGGCGCCCGCGCGCGCGCTTCGAGTCCGGACTCG
-----+-----+-----+-----+-----+-----+-----+-----+
GCGACGAGGCGCCAGGAGCGCTCCGGGGCGGGCGGGCGGGAAGCTCAGGCCTGAGC
L L P G P R E A P A A A A A F E S G L D
180
ACCTCTCGGACGCGGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAAGATCTGG
-----+-----+-----+-----+-----+-----+-----+-----+
TGGAGAGCCTCGCGCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTCTGTTCTAGACC
L S D A E P D A G E A T A Y A S K D L E
240
AGGAGCAGTTACGGTCTGTGTCCAGTGATGAATCATGACTGTACTCTACCCAGAAT
-----+-----+-----+-----+-----+-----+-----+-----+
TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGTCTTA
E Q L R S V S S V D E L M T V L Y P E Y
300
ATTGGAAAATGTACAAGTGTGCTAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG
-----+-----+-----+-----+-----+-----+-----+-----+
TAACCTTTTACATGTTACAGTCGATTCTTCTCCGACCGTGTGATTTGTCTCTGTGTC
W K M Y K C Q L R K G G W Q H N R E Q A
360
CCAACCTCAACTCAAGGACAGAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG
-----+-----+-----+-----+-----+-----+-----+-----+
GGTTGGAGTTGAGTTCCTGTCTCTCTGATATTTAAACGACGTCGTGTAATATATGTC
N L N S R T E E T I K F A A A H Y N T E

FIG. 1A



2/ 20

361 AGATCTTGAAAAGTATTGATAAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
-----+-----+-----+-----+-----+-----+-----+
TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
I L K S I D N E W R K T Q C M P R E V C
420

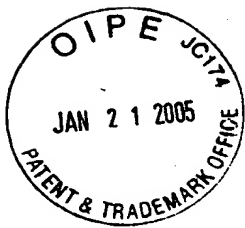
421 GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
-----+-----+-----+-----+-----+-----+-----+
CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTGTGGAAGAAATTTGGAGGTACAC
I D V G K E F G V A T N T F F K P P C V
480

481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
-----+-----+-----+-----+-----+-----+-----+
ACAGGCAGATGTCTACACCCCCCAACGACGTTATCATTACCTCCCGACGTCACGTACTTGTGGT
S V Y R C G G C C N S E G L Q C M N T S
540

541 GCACGAGCTACCTCAGCAAGACGTTATTGAAATTACAGTGCCCTCTCTCTCAAGGCCCCA
-----+-----+-----+-----+-----+-----+-----+
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTACGGAGAGAGAGTTCCTGGGGT
T S Y L S K T L F E I T V P L S Q G P K
600

601 AACCAGTAACAATCAGTTTTTGCCCAATCACACTTCTCTGCCGATGCATGTCTAAACTGGATG
-----+-----+-----+-----+-----+-----+-----+
TTGGTCATTGTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC
P V T I S F A N H T S C R C M S K L D V
660

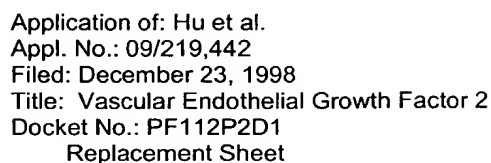
FIG. 1B



3/ 20

661 TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
720 -----+-----+-----+-----+-----+-----+-----+
AAATGCTCTGTTCAAGGTAAGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACACAG
Y R Q V H S I I R R S L P A T L P Q C Q
780 AGGCAGCGAACAAGACCTGCCCCCACCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
-----+-----+-----+-----+-----+-----+-----+
TCCGTCGCTTGTCTCGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTTCTACGG
A A N K T C P T N Y M W N N H I C R C L
840 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
-----+-----+-----+-----+-----+-----+-----+
ACCGAGTCCTTCTAAAATACAAAAGGAGCCCTACGACCTCTACTGAGTTGTCTACCTAAGG
A Q E D F M F S S D A G D D S T D G F H
900 ATGACATCTGTGGACCAACAAGAGCTGGATGAAGAGACCTGTCAAGTGTGTCTGCAGAG
-----+-----+-----+-----+-----+-----+-----+
TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
D I C G P N K E L D E E T C Q C V C R A
960 CGGGGCTTCGGCCCTGCCAGCTGTGGACCCCCACAAAGAACTAGACAGAAACTCATGCCAGT
-----+-----+-----+-----+-----+-----+-----+
GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTACGGTCA
G L R P A S C G P H K E L D R N S C Q C

FIG. 1C



1020

CACAGACATTTTGTGAGAAGGGTCGGTTACACCCCGGTGGCTCTTAACA

961

1080

ACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTCGGAA
 TGTGTACGGTCACACATACATTTCTTGGACGGGGTCTTTAGTTGGGATTTAGGACCTT
 T C C Q C C V C K R T C P R N Q P L N P G K

1021

1140

AAATGTGCGCTGTGAATGTACAGAAAGTCCACAGAAAATGCTTGTTAAAGGAAAGAAGTTCC
-----+-----+-----+-----+-----+-----+-----
TTTACACGGACACTTACATGTCTTTTCAGGTGCTTTACGAACAATAATTTCTTCTTCAAGG
C A C E C T E S P Q K C L K G K K F H

1081

1200

ACCAACCAACATGCAGCTGTTACAGACGGCCATGTACGAACCCAGAAAGGCTTGTGAGC
TGGTGGTTGTACGTCGACAATGCTGCCGGTACATGCTTGGGGTCTTCCGAACACTCG
H O T C S C Y R R P C T N R Q K A C E P

1141

1260

CAGGATTTTCATATAGTGAAGAAGTGTCGTGTGTGCCCTTCATATTGGCAAAGACCCAC
-----+-----+-----+-----+-----+-----+-----+
GTCCATAAAGTATATCACTTCTTCACACAGCAACAACAGGGAAAGTATAACCGTTTCTGGTG
G F S Y S E E V C R C V P S Y W Q R P Q

1201

FIG. 1D



1320
AAATGAGCTAAGATTGTACTGTGTTTTCCAGTTTCATCGATTTTCTATTATGGAACCTGTGT
-----+-----+-----+-----+-----+-----+-----+
TTTACTCGATTCTTAACATGACACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGGACACA
M S *
1380
TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCCTTGTGGGTCCATGCTAACAAAGACA
-----+-----+-----+-----+-----+-----+-----+
ACGGTGTCACTTGACAGACACTTGTCTCTCTGGAACACCCAGGTACGATTGTTTCTGT
1440
AAAGTCTGTCTTCCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
-----+-----+-----+-----+-----+-----+-----+
TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCCTTACCTGACCTCGAGTAGAC
1500
CAAAAGGCCCTCTTGTAAGACTGGTTTCTGCGCAATGACCAAAACAGCAAGATTTTCCCTC
-----+-----+-----+-----+-----+-----+-----+
GTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCTGGTTCTTAAAGGAG
1560
TTGTGATTTCTTTAAAGAAATGACTATATAATTTATTTCCACTAAAAAATATTGTTTCTGC
-----+-----+-----+-----+-----+-----+-----+
AACACTAAAGAAATTTTCTTACTGATATATTAATAAAGGTGATTTTATTAACAAAGACG
1620
ATTCATTTTATAGCAACAACAATGGTAAACCTCAGTGTGATCAATATTTTATATCAT
-----+-----+-----+-----+-----+-----+-----+
TAAGTAAAAAATATCGTTGTTGTTAAACCAATTTTGAGTGACACTAGTTATAAAAAATATAGTA
1674
GCAAAATATGTTTAAATAAAATGAAAATTTGATTTTATATAAAAAA
-----+-----+-----+-----+-----+-----+-----+
CGTTTATACAAATTTTATTTTACTTTTAAACATAAATAATTTTATTTT

FIG. 1E



6/ 20

1 CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+
61 AGATGAACATCATGACTGTACTCTACCCAGAATATTGGAAAAATGTACAAGTGTCAAGCTAAG
-----+-----+-----+-----+-----+-----+-----+
M T V L Y P E Y W K M Y K C Q L R
-----+-----+-----+-----+-----+-----+-----+
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAGAGAC
-----+-----+-----+-----+-----+-----+-----+
K G G W Q H N R E Q A N L N S R T E E T
-----+-----+-----+-----+-----+-----+-----+
181 TATAAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAAGTATTGATAATGAGTG
-----+-----+-----+-----+-----+-----+-----+
I K F A A A H Y N T E I L K S I D N E W
-----+-----+-----+-----+-----+-----+-----+
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
-----+-----+-----+-----+-----+-----+-----+
R K T Q C M P R E V C I D V G K E F G V
-----+-----+-----+-----+-----+-----+-----+
301 CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG
-----+-----+-----+-----+-----+-----+-----+
A T N T F F K P P C V S V Y R C G G C C
-----+-----+-----+-----+-----+-----+-----+

FIG. 2A



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421 TGAAATTACAGTGCCTCTCTCTCAAGGCCCAACCAAGTAACAATCAGTTTGGCCAATCA
E I T V P L S Q G P K P V T I S F A N H
481 CACTTCCTGCCGATGCATGCTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
T S C R C M S K L D V Y R Q V H S I I R
541 ACGTTCCTGCCAGCAACACTACCACAGTGTCTCAGGCAGCGAACAAGACCTGCCCCACCAA
R S L P A T L P Q C Q A A N K T C P T N
601 TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTATGTTTTCCTC
Y M W N N H I C R C L A Q E D F M F S S
661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAACAAGGAGCT
D A G D D S T D G F H D I C G P N K E L
721 GGATGAAGAGACCTGTGAGTGTCTGCAGAGCGGGCTTCGGCTGCCAGCTGTGGACC
D E E T C Q C V C R A G L R P A S C G P

FIG. 2B



781 CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAACAACTCTTCCCCAG
H K E L D R N S C Q C V C K N K L F P S

841 CCAATGTGGGGCCCAACCGAATTTGATGAAAAACACATGCCAGTGTGTATGTAAAAAGAAC
Q C G A N R E F D E N T C Q C V C K R T

901 CTGCCCCAGAAATCAACCCCTAAATCTCTGGAAAAATGTGCCTGTGAATGTACAGAAAGTCC
C P R N Q P L N P G K C A C E C T E S P

961 ACAGAAATGCTTGTAAAGGAAAGAAAGTTCCACCACCAACATGCAGCTGTTACAGACG
Q K C L L K G K K F H H Q T C S C Y R R

1021 GCCATGTACGAACCGCCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
P C T N R Q K A C E P G F S Y S E E V C

1081 TCGTTGTCCCTTCATATTGGCAAGACCAACACAAATGAGCTAAGATTGTACTGTTTCCCA
R C V P S Y W Q R P Q M S *

FIG. 2C



9/ 20

1141 GTTCATCGATTTTCTATTATGGAAGAACTGTGTGCCACAGTAGAACTGTCTGTGAACAGA
-----+-----+-----+-----+-----+-----+-----+
1201 GAGACCCTTGTGGTCCATGCTAACAAAGACAAAAGTCTGTCTTTCTCTGAACCATGTGGA
-----+-----+-----+-----+-----+-----+-----+
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCCTCTTGTAAAGACTGGTTT
-----+-----+-----+-----+-----+-----+-----+
1321 CTGCCAATGACCCAAACAGCCCAAGATTTCCTCTTGTGATTTCCTTAAAGAAATGACTATA
-----+-----+-----+-----+-----+-----+-----+
1381 TAATTTATTTCCACTAAAATATTGTTTCTGCATTCAATTTTATAGCAACAACAATTGGT
-----+-----+-----+-----+-----+-----+-----+
1441 AAAACTCACTGTGATCAATATTTTATATCATGCAGCAAAATATGTTTAAATAAAATGAAAA
-----+-----+-----+-----+-----+-----+-----+
1501 TTGTATTATATAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+

FIG. 2D